



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 856 723

Source: OIEP

Date Processed by STIC: 10/03/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/856723
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,723

DATE: 10/03/2001

TIME: 15:30:54

Input Set : A:\sequence listing 856723.7sept01.txt

Output Set: N:\CRF3\10032001\I856723.raw

3 <110> APPLICANT: Kramer, Michael  
 5 <120> TITLE OF INVENTION: Regulatory Protein pKe#83 from Human  
 6 Keratinocytes  
 8 <130> FILE REFERENCE: km-3/PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/856,723  
 C--> 11 <141> CURRENT FILING DATE: 2001-09-17  
 13 <150> PRIOR APPLICATION NUMBER: DE19854672.6  
 14 <151> PRIOR FILING DATE: 1998-11-26  
 16 <150> PRIOR APPLICATION NUMBER: DE19856301.9  
 17 <151> PRIOR FILING DATE: 1998-12-07  
 19 <160> NUMBER OF SEQ ID NOS: 10  
 21 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
 Corrected Diskette Needed

Error: unknowns in line 599  
 must enumerate unknowns

## ERRORED SEQUENCES

"n" in a sequence must be described  
 in fields 221, 222, and 223

512 <210> SEQ ID NO: 7  
 513 <211> LENGTH: 4914  
 514 <212> TYPE: DNA  
 515 <213> ORGANISM: Homo sapiens  
 517 <400> SEQUENCE: 7  
 518 ggcgggggag cctccagaa taccatcat atagccctg aggtggcatg gtgatgtctc 60  
 519 catgaggga ccccttccca cttcatactg tcacgtatat catagtgttc ttgactgggc 120  
 520 cattcatcta agatgggatt taccctgtga aacagggaga agacttatgg accccaagca 180  
 521 tcatttcaag ttgaagtga gtttttaaaa gccatccatg caaagttcct ttgctttgga 240  
 522 cctctgcat tattaagct gctgtattgc taaccagaa ctgctccagt gtcttgactg 300  
 523 atcatcatgg cttcagtttg gaagagactg cagcgtgtgg gaaaacatgc atccaagttc 360  
 524 cagtttgttg cctcctacca ggagctcatg gttgagtgtg cgaagaaatg gtaaccagat 420  
 525 aaactgggtg tagtttggac cagaagaagc cgaaggaaat cttctaaggc acatagctgg 480  
 526 caacctggaa taaaaaatcc ctatcgtggg gttgttgtgt ggccgtgttc tgaaaacatt 540  
 527 gaaatcactg taacactttt taaggatcct catgcggaag aatttgaaga caaagagtgg 600  
 528 acatttgtca tagaaaatga atcccttctt ggtcgaagga aagctcttgc tactagcagc 660  
 529 atcaatatga aacagtatgc aagccctatg ccaactcaga ctgatgtcaa gttaaaattc 720  
 530 aagccattat ctaaaaaagt tgtatctgcc gctcttcagt ttccattatc ttgcattttt 780  
 531 ctgaggggaag gaaaagccac agatgaagac atgcaaagtt tggctagttt ggtgagtatg 840  
 532 aagcaggctg acattggcaa ttagatgac ttcgaagaag ataatagaaga tgatgatgag 900  
 533 aacagagtga accaagaaga aaaggcagct aaaattacag agcttatcaa caaacttaac 960  
 534 tttttggatg aagcagaaaa ggacttggcc accgtgaatt caaatccatt tgatgatcct 1020  
 535 gatgctgcag aattaaatcc atttggagat cctgactcag aagaacctat cactgaaaca 1080  
 536 gcttcacctg gaaaaacaga agactctttt tataataaca gctataatcc ctttaaagag 1140  
 537 gtgcagactc cacagtattt gaacccattc gatgagccag aagcatttgt gaccataaag 1200  
 538 gattctcttc ccagctctac aaaaagaaaa aatataagac ctgtggatat gagcaagtac 1260  
 539 ctctatgctg atagtcttaa aactgaagaa gaagaattgg atgaatcaaa tcttttttat 1320  
 540 gaacctaaat caactcctcc tccaaataat ttggtaaatc ctgttcaaga actagaaact 1380  
 541 gaaaggcgag tgaaaagaaa ggccccggct ccaccagtc tctcaccaaa aacaggagta 1440  
 542 ttaaatgaaa acacagtttc tgcaggaaaa gatctctcta cttctcttaa gccaaagcct 1500  
 543 ataccaagtc ctgttttggg gcgaaagcca aatgctagtc agtctttgct tgtatggtgt 1560

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```

544 aaagaagtta caaagaacta ccgaggagta aaaatcacca attttactac atcgtggaga 1620
545 aatggtttat ctttttgtgc aatattacac cacttttagac cagatttaat tgactacaag 1680
546 tctctgaatc ctcaagatat taaagagaac aacaaaaagg catacgatgg atttgccagc 1740
547 ataggaatth cccgattatt ggaaccttct gatatggtat tattagcaat tcctgataaa 1800
548 ctgactgtta tgacttatct ctatcaaata agggcacatt tcagtggcca agaactaaat 1860
549 gtcgttcaga tagaggaaaa cagcagtaaa agcacatata aagttggaaa ctatgaaaca 1920
550 gatacaaaaca gttctgttga tcaagaaaaa ttctatgcag agcttagtga tctgaagcgg 1980
551 gagcctgaac tacaacagcc tatcagcggg gcagtagact tcttatcaca ggatgactct 2040
552 gtatttghta atgatagcgg ggttggagag tcagaaagtg agcatcaaac tcctgatgat 2100
553 caccctagtc caagcacagc ctccccttac tgcgcagga ctaaaagtga cacagaaccc 2160
554 cagaagtctc agcacagctc tggaaggact tcaggatctg atgaccctgg aatatgttcc 2220
555 aatacagatt caaccaagc acaggttttg ttaggcaaaa agagactatt gaaagctgag 2280
556 actttagaat tgagtgaact atatgttagt gataagaaga aggatatgtc tccacctttt 2340
557 atttgtgagg agacagatga acaaaagctt caaactctag acatcggtag taacttggag 2400
558 aaagaaaaat tagagaattc cagatcctta gaatgcagat cagatccaga atctcctatc 2460
559 aaaaaaacia gtttatctcc tacttctaaa cttggatact catatagtag agatctagac 2520
560 cttgctaaga aaaaacatgc ttccctgagg cagacggagt ctgatccaga tgctgataga 2580
561 accactttta atcatgcaga tcattcatca aaaatagctc agcatcgatt gttatctaga 2640
562 caagaagaac ttaaggaaag agcaagagtt ctgcttgagc aagcaagaag agatgcagcc 2700
563 ttaaaggcgg ggaataagca caataccaac acagccacc cttctgcaa caggcagcta 2760
564 agtgatcagc aagatgaaga gcgacgtcgg cagctgagag agagagctcg tcagctaata 2820
565 gcagaagctc gatctggagt gaagatgtca gaacttccca gctatggtga aatggctgca 2880
566 gaaaagttga aagaaaggtc aaaggcatct ggagatgaaa atgataatat tgagatagat 2940
567 actaacgagg agatccctga aggctttgtt gtaggaggtg gagatgaact tactaactta 3000
568 gaaaatgacc ttgatactcc cgaacaaaac agtaagttgg tggacttgaa gctgaagaag 3060
569 ctcttagaag ttcagccaca ggtggcaaat tcacctcca gtgctgcca gaaagctgta 3120
570 actgagagct cagagcagga catgaaaagt ggcacagaag atctccggac tgaacgatta 3180
571 caaaaaacia cagaacgttt tagaaatcct gttgtgttca gcaaagattc tacagtcaga 3240
572 aaaactcaac ttcagctctt cagccaatat attgagaata gaccagagat gaaaaggcag 3300
573 agatcaatac aggaagatac aaagaaagga aatgaggaga aggcagcgat aactgaaact 3360
574 cagaggaagc catcagaaga tgaagtgtt aataaaggtt tcaaagacac cagtcagtat 3420
575 gtagtaggag aattggcagc actagagaat gagcaaaagc aaattgacac ccgtgccgcg 3480
576 ctggtggaga agcgccttcg ctatctcatg gacacaggaa ggaacacaga agaagaagaa 3540
577 gctatgatgc aggaatggtt tatgttagtt aataagaaaa atgccttaat aaggagaatg 3600
578 aatcagctct ctcttctgga aaaagaacat gatttagaac gacggtatga gctgctgaac 3660
579 cgggaattga gggcaatgct agccattgaa gactggcaga agaccgaggc ccagaagcga 3720
580 cgcgaacagc ttctgctaga tgagctggtg gccctggtga acaagcgcga tgcgctcgtc 3780
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582 ctggagcaaa acaaaggcaa gatggccaag aaagaggaga aatgtgttct tcagtagcca 3900
583 tcagatcaga aagaatctct cccaacattt tagagtcttg ctccccaaac cagaaaaagt 3960
584 cagactcatt gttgatttaa aacttttaac attttgtttg gctggattgt actactttac 4020
585 ctctacttta ccaccaccac ccttttctc cctcctttcc aaataatata cagaactcca 4080
586 aaatagcttc atttaaggat ttttttgtga gttacaatt tccttgaaat cctgtgaaat 4140
587 agatttgcac agacaccttg tgagtgattg gtattggagg tgttcaagaa actgttcgaa 4200
588 aagaacaaa aacacttccc tcgttatatt ctctcatttt ttgatgagag gaaaatttga 4260
589 aacattattc ttgtgtttgt tggtaatagc ataatgacag tgggaggggt acaaggggat 4320
590 aagaaaaatg tcatgatttt ttccggctcc tgccacatgt aacacttact ctgttaccta 4380
591 aattttatag ttagatcata tccaatctac ttattaaact gtgttctatt taccagtggg 4440
592 gtttttctgc agtggttgcg tttcactgta aggataatgg agttcctctc ctctgctttc 4500

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593 ctacagaggat ggtccttttaa catagccaga aacaagccct gtggtttgaa ggtgagctgt 4560  
594 gaggatggga ctaattgata tgcaccagtt tacaaagaca gtcttatcat ccgagaatac 4620  
595 accatctttt tctctggata attatttctt acatcatgct tgattctac attttggttg 4680  
596 gtttcaacat tggctcacga atgctgttaa tatttattct gtattgataa aaagtctgtc 4740  
597 ttgccactac aagtaaattcc cccatttaatt attttcttct ttagcatagc actgtcattt 4800  
598 tttgtgaaaa tggttatggt tatttattac aatactgagt catatatataa ttttcaataa 4860  
E--> 599 aagcagaaac tttcttacct taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aad 4914

↓  
invalid

## VERIFICATION SUMMARY

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Input Set : A:\sequence listing 856723.7sept01.txt

Output Set: N:\CRF3\10032001\I856723.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:599 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7  
L:599 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1